

The Filiformis (Fil) locus is found to be allelic to reductus

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Introduction

The gene *reductus* (*red1*) was first reported by Winge in 1936 (1) as reducing the size of leaflets by 65–90% while also reducing the size of stipules but to a lesser degree. Lamprecht later published on the gene *maximo-reductus* (*mare*) with similar phenotype (2, 3). In 1976 Marx confirmed allelism between *mare* and *red1* which resulted in *red* being accepted as the valid gene symbol and the symbol *mare* was discontinued (3). Two further induced mutants at the *red1* locus have subsequently been isolated by Rozov (4).

Recent observations on an induced mutation (WL 5143 *flagellarius*) reported by Stig Blixt showed a similar but more severe and earlier reduction in the size of leaflets and stipules than witnessed in the alleles of *red1-1*, *red1-2*, *red1-3*, with these becoming tread like after the first 3 nodes (Fig. 1a). This phenotype was noted as bearing a striking similarity to an induced mutant reported by Monti (5) as *filiformis*, *fil* in Parvus (Fig. 1b) which was described as exhibiting strong modification of leaflets and flowers with leaflets and stipules becoming progressively reduced until threadlike.

Figure 1. Phenotypes of mutants of a. WL 5143 *flagellarius* b. Mutant P 674 (*filiformis*). Photograph by Stig Blixt.



A further induced *filiformis* mutant (WL 5946) isolated again by Stig Blixt was noted in the Nordic collection but had not been the subject of any reported allelism study. Allelism tests were therefore conducted between these mutants and *redl* mutants to explore their relationships and interactions.

Results

Two of the mutants (WL 5143 and WL 5946) were crossed directly as the pollen was fertile. This is not the case for JI 2181 which is maintained as a heterozygous line. Crosses were performed to 9 JI 2181 plants, of which 3 were revealed to be heterozygous by progeny tests. The results of the allelism tests are presented in Table 1 which revealed all the three mutants to be allelic to *redl*.

Table 1. Allelism tests between mutants and JI 802 (*redl-1*).

Cross	F1 plants	Phenotype of F1 plants
JI 802 x WL 5143	4	All of mutant phenotype
JI 802 X WL 5946	3	All of mutant phenotype
JI 802 X JI 2181 (potential hets)	14	8/14 of mutant phenotype

In the course of these studies all mutants, with the exception of JI 2181 produced viable pollen, confirming the findings of Monti (5). The anthers of JI 2181 homozygous mutants develop, but they fail to produce pollen. A summary of the lines and their pollen and fertility status is presented in Table 2.

Table 2. Table of *reductus* mutants confirmed through allelism tests.

Line number	JI no.	Mutagen	Year	Initial line	Pollen viable	Fertile	Former gene symbol	Valid gene symbol
Winge 37 (WL 449)	802	Spont.	1936		yes	yes	<i>red</i>	<i>redl-1</i>
XCIM4M (WL 1674)	833	Spont.	1967		yes	yes	<i>mare</i>	<i>redl-2 (new)</i>
SG 0634	3058	EMS	1997	SG	yes	yes	<i>redl-2</i>	<i>redl-3 (new)</i>
SG 0404	3254	EMS	1997	SG	yes	yes	<i>redl-3</i>	<i>redl-4 (new)</i>
WL 5143 (<i>flagellarius</i>)	3514			W709	yes	yes		<i>redl-5 (new)</i>
P 674g	2181	DES	1970	Parvus	no	no	<i>fil</i>	<i>redl-6 (new)</i>
WL 5946 (<i>filiformis</i>)	3552	EMS		Parvus	yes	no		<i>redl-7(new)</i>

Discussion

The severe reduction in leaf and stipule area in mutants of *filiformis* and *flagellarius* have been shown to be allelic to *redl* mutants. The *Redl* locus, having been established earlier, has precedence over *Fil* which is no longer considered a valid symbol but a synonym for *Redl*. Three new alleles have thus been added to the *redl* series bringing the total number of known alleles at this locus to 7. This study provides a useful point at which to revise the extended series of alleles. This is required to overcome the problem of the alleles identified by Rozov (4) as being numbered with reference to only one of the earlier alleles rather than the two resulting from the investigations by Marx (3). The proposed renumbering of the alleles presented in Table 2 follows the sequence in which they were established as *redl* alleles in the literature.

With the exception of *redl-3* and *redl-4*, the remaining four mutant alleles are present in widely different parental backgrounds preventing any close comparison of the phenotypic severity of these alleles. A backcross programme is currently underway using JI 2822 as the recurrent parent in order to generate near-isogenic lines for each of the mutant alleles so that the differences in severity of each allele can be more easily studied.

1. Winge, O. 1936. Comptes rendus des travaux du Laboratoire Carlesberg, 21: 271-393.
2. Lamprecht H. 1967. Phytion 12: 252-265.
3. Marx, G.A. 1976. *Pisum* Newsletter 8:39.
4. Rozov, S.M., Gorel, F.L. and Berdnikov V.A. 1997. *Pisum* Genetics 29: 44-46.
5. Monti, L.M. 1970. *Pisum* Newsletter 2: 21.